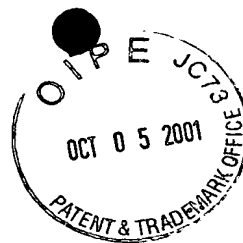


SEQUENCE LISTING



<110> MOLONEY, MAURICE M.
DALMIA, BIPIN K.

<120> PREPARATION OF THIOREDOXIN AND THIOREDOXIN REDUCTASE
PROTEINS ON OIL BODIES

<130> 034547/0106

<140> 09/897,425

<141> 2001-07-03

<150> 09/210,843

<151> 1998-12-18

<150> 08/846,021

<151> 1997-04-25

<150> 08/366,783

<151> 1994-12-30

<150> 08/142,418

<151> 1993-11-16

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tcgtcgggtc cttgggcat tgcggcgga gatgggtcag cttgggcttg aggacgagac 180
ccgaatcgag tctgttgaaa ggttggtcat tgggatttgt atacggagat tggtcgtcga 240
gaggtttgag ggaaaggaca aatgggtttg gctctggaga aagagagtgc ggcttttagag 300
agagaattga gaggtttaga gagagatgcg gcggcgatga cgggaggaga gacgacgagg 360

acg gga gag cac cca cag gga tca gac aag ttg gac agt gca agg atg 1515
 Thr Gly Glu His Pro Gln Gly Ser Asp Lys Leu Asp Ser Ala Arg Met
 125 130 135

 aag ttg gga agc aaa gct cag gat ctg aaa gac aga gct cag tac tac 1563
 Lys Leu Gly Ser Lys Ala Gln Asp Leu Lys Asp Arg Ala Gln Tyr Tyr
 140 145 150

 gga cag caa cat act ggt ggg gaa cat gac cgt gac cgt act cgt ggt 1611
 Gly Gln Gln His Thr Gly Gly Glu His Asp Arg Asp Arg Thr Arg Gly
 155 160 165

 ggc cag cac act act taagttaccc cactgatgtc atcgatcatag tccaataact 1666
 Gly Gln His Thr Thr
 170

 ccaatgtcgg ggagttagtt tatgaggaat aaagtgttta gaatttgatc aggggggagat 1726

 aataaaagcc gagtttgaat ctttttgtta taagtaatgt ttatgtgtgt ttctatatgt 1786

 tgtcaaattgg tacc 1800

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 <213> Arabidopsis thaliana

<400> 2
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 Gln Tyr Pro Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met Ser Gly
 20 25 30

 Arg Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr
 35 40 45

 Ala Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu
 50 55 60

 Val Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile
 65 70 75 80

 Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile
 85 90 95

 Thr Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val
 100 105 110

 Phe Ser Trp Ile Tyr Lys
 115

<210> 3
 <211> 55
 <212> PRT
 <213> Arabidopsis thaliana

<400> 3

Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp Lys Leu Asp Ser Ala
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 Arg Met Lys Leu Gly Ser Lys Ala Gln Asp Leu Lys Asp Arg Ala Gln
 20 25 30
 Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp Arg Asp Arg Thr
 35 40 45
 Arg Gly Gly Gln His Thr Thr
 50 55

<210> 4

<211> 564

<212> DNA

<213> Brassica napus

<220>

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<222> (1)..(561)

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 1 5 10 15
 tat ccc cga gac cga gac cag tat tct atg atc ggt cga gac cgt gac 96
 Tyr Pro Arg Asp Arg Asp Gln Tyr Ser Met Ile Gly Arg Asp Arg Asp
 20 25 30
 cag tac tct atg atg ggc cga gac cga gac cag tac aac atg tat ggt 144
 Gln Tyr Ser Met Met Gly Arg Asp Arg Asp Gln Tyr Asn Met Tyr Gly
 35 40 45
 cga gac tac tcc aag tct aga cag att gct aag gct gtt acc gca gtc 192
 Arg Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Val Thr Ala Val
 50 55 60
 acg gcg ggt ggg tcc ctc ctt gtc ctc tcc agt ctc acc ctt gtt ggt 240
 Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu Val Gly
 65 70 75 80
 act gtc att gct ttg act gtt gcc act cca ctc ctc gtt atc ttt agc 288
 Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile Phe Ser
 85 90 95
 cca atc ctc gtg ccg gct ctc atc acc gta gca ctt ctc atc act ggc 336
 Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile Thr Gly
 100 105 110
 ttt ctc tcc tct ggt ggg ttt gcc att gca gct ata acc gtc ttc tcc 384
 Phe Leu Ser Ser Gly Gly Phe Ala Ile Ala Ala Ile Thr Val Phe Ser
 115 120 125

tgg atc tat aag tac gca acg gga gag cac cca cag ggg tca gat aag 432
 Trp Ile Tyr Lys Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp Lys
 130 135 140

ttg gac agt gca agg atg aag ctg gga acc aaa gct cag gat att aaa 480
 Leu Asp Ser Ala Arg Met Lys Leu Gly Thr Lys Ala Gln Asp Ile Lys
 145 150 155 160

gac aga gct caa tac tac gga cag caa cat aca ggt ggt gag cat gac 528
 Asp Arg Ala Gln Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp
 165 170 175

cgt gac cgt act cgt ggt ggc cag cac act act taa 564
 Arg Asp Arg Thr Arg Gly Gly Gln His Thr Thr
 180 185

<210> 5

<211> 187

<212> PRT

<213> Brassica napus

<400> 5

Met Ala Asp Thr Ala Arg Thr His His Asp Val Thr Ser Arg Asp Gln
 1 5 10 15

Tyr Pro Arg Asp Arg Asp Gln Tyr Ser Met Ile Gly Arg Asp Arg Asp
 20 25 30

Gln Tyr Ser Met Met Gly Arg Asp Arg Asp Gln Tyr Asn Met Tyr Gly
 35 40 45

Arg Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Val Thr Ala Val
 50 55 60

Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu Val Gly
 65 70 75 80

Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile Phe Ser
 85 90 95

Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile Thr Gly
 100 105 110

Phe Leu Ser Ser Gly Gly Phe Ala Ile Ala Ala Ile Thr Val Phe Ser
 115 120 125

Trp Ile Tyr Lys Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp Lys
 130 135 140

Leu Asp Ser Ala Arg Met Lys Leu Gly Thr Lys Ala Gln Asp Ile Lys
 145 150 155 160

Asp Arg Ala Gln Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp
 165 170 175

Arg Asp Arg Thr Arg Gly Gly Gln His Thr Thr
 180 185

<210> 6
 <211> 2733
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fragment of
 pSBSOTPTNT containing the oleosin-chymosin fusion
 gene

<220>
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 <222> (850)..(1203)

<220>
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 attgcggcgg aagatgggtc agcttgggct tgaggacgag acccgaatcg agtctgttga 180
 aaggttgttc attgggattt gtatacggag attggctcgtc gagaggtttg agggaaagga 240
 caaatggggtt tggtctctgga gaaagagagt gcggcctttag agagagaatt gagaggttta 300
 gagagagatg cggcggcgat gacgggagga gagacgacga ggacctgcat tatcaaagca 360
 gtgacgtggt gaaatttgga acttttaaga ggcagataga tttattattt gtatccattt 420
 tcttcattgt tctagaatgt cgcggaacaa attttaaaac taaatcctaa atttttctaa 480
 ttttggtgcc aatagtggat atgtggggccg tatagaagga atctattgaa ggcccaaacc 540
 catactgacg agcccaaagg ttcgttttgc gttttatggt tcggttcgat gccaacgcca 600
 cattctgagc taggcaaaaa acaaacgtgt ctttgaatag actcctctcg ttaacacatg 660
 cagcggctgc atggtgacgc cattaacacg tggcctacaa ttgcatgatg tctccattga 720
 cacgtgactt ctctgtctct ttcttaatat atctaacaaa cactcctacc tcttccaaaa 780
 tatatacaca tctttttgat caatctctca ttcaaaatct cattctctct agtaaacaag 840
 aacaaaaaa atg gcg gat aca gct aga gga acc cat cac gat atc atc ggc 891
 Met Ala Asp Thr Ala Arg Gly Thr His His Asp Ile Ile Gly
 1 5 10
 aga gac cag tac ccg atg atg ggc cga gac cga gac cag tac cag atg 939
 Arg Asp Gln Tyr Pro Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met
 15 20 25 30

tcc gga cga gga tct gac tac tcc aag tct agg cag att gct aaa gct	987
Ser Gly Arg Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala	
35 40 45	
gca act gct gtc aca gct ggt ggt tcc ctc ctt gtt ctc tcc agc ctt	1035
Ala Thr Ala Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu	
50 55 60	
acc ctt gtt gga act gtc ata gct ttg act gtt gca aca cct ctg ctc	1083
Thr Leu Val Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu	
65 70 75	
gtt atc ttc agc cca atc ctt gtc ccg gct ctc atc aca gtt gca ctc	1131
Val Ile Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu	
80 85 90	
ctc atc acc ggt ttt ctt tcc tct gga ggg ttt ggc att gcc gct ata	1179
Leu Ile Thr Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile	
95 100 105 110	
acc gtt ttc tct tgg att tac aag taagcacaca tttatcatct tacttcataa	1233
Thr Val Phe Ser Trp Ile Tyr Lys	
115	
ttttgtgcaa tatgtgcatg catgtgttga gccagtagct ttggatcaat ttttttggtc	1293
gaataacaaa tgtaacaata agaaattgca aattctaggg aacatttggt taactaaata	1353
cgaaatttga cctagctagc ttgaatgtgt ctgtgtatat catctatata ggtaaaatgc	1413
ttggtatgat acctattgat tgtgaatagg tac gca acg gga gag cac cca cag	1467
Tyr Ala Thr Gly Glu His Pro Gln	
120 125	
gga tca gac aag ttg gac agt gca agg atg aag ttg gga agc aaa gct	1515
Gly Ser Asp Lys Leu Asp Ser Ala Arg Met Lys Leu Gly Ser Lys Ala	
130 135 140	
cag gat ctg aaa gac aga gct cag tac tac gga cag caa cat act ggt	1563
Gln Asp Leu Lys Asp Arg Ala Gln Tyr Tyr Gly Gln Gln His Thr Gly	
145 150 155	
ggg gaa cat gac cgt gac cgt act cgt ggt ggc cag cac act act ctc	1611
Gly Glu His Asp Arg Asp Thr Arg Gly Gly Gln His Thr Thr Leu	
160 165 170	
gtt cca cga gga tcc atg gct gag atc acc agg atc cct ctg tac aaa	1659
Val Pro Arg Gly Ser Met Ala Glu Ile Thr Arg Ile Pro Leu Tyr Lys	
175 180 185 190	
ggc aag tct ctg agg aag gcg ctg aag gag cat ggg ctt ctg gag gac	1707
Gly Lys Ser Leu Lys Ala Leu Lys Glu His Gly Leu Leu Glu Asp	
195 200 205	
ttc ctg cag aaa cag cag tat ggc atc agc agc aag tac tcc ggc ttc	1755
Phe Leu Gln Lys Gln Gln Tyr Gly Ile Ser Ser Lys Tyr Ser Gly Phe	
210 215 220	

ggg gag gtg gcc agc gtg ccc ctg acc aac tac ctg gat agt cag tac	1803
Gly Glu Val Ala Ser Val Pro Leu Thr Asn Tyr Leu Asp Ser Gln Tyr	
225 230 235	
ttt ggg aag atc tac ctc ggg acc ccg ccc cag gag ttc acc gtg ctg	1851
Phe Gly Lys Ile Tyr Leu Gly Thr Pro Pro Gln Glu Phe Thr Val Leu	
240 245 250	
ttt gac act ggc tcc tct gac ttc tgg gta ccc tct atc tac tgc aag	1899
Phe Asp Thr Gly Ser Ser Asp Phe Trp Val Pro Ser Ile Tyr Cys Lys	
255 260 265 270	
agc aat gcc tgc aaa aac cac cag cgc ttc gac ccg aga aag tcg tcc	1947
Ser Asn Ala Cys Lys Asn His Gln Arg Phe Asp Pro Arg Lys Ser Ser	
275 280 285	
acc ttc cag aac ctg ggc aag ccc ctg tct atc cac tac ggg aca ggc	1995
Thr Phe Gln Asn Leu Gly Lys Pro Leu Ser Ile His Tyr Gly Thr Gly	
290 295 300	
agc atg cag ggc atc ctg ggc tat gac acc gtc act gtc tcc aac att	2043
Ser Met Gln Gly Ile Leu Gly Tyr Asp Thr Val Thr Val Ser Asn Ile	
305 310 315	
gtg gac atc cag cag aca gta ggc ctg agc acc cag gag ccc ggg gac	2091
Val Asp Ile Gln Gln Thr Val Gly Leu Ser Thr Gln Glu Pro Gly Asp	
320 325 330	
gtc ttc acc tat gcc gaa ttc gac ggg atc ctg ggg atg gcc tac ccc	2139
Val Phe Thr Tyr Ala Glu Phe Asp Gly Ile Leu Gly Met Ala Tyr Pro	
335 340 345 350	
tcg ctc gcc tca gag tac tcg ata ccc gtg ttt gac aac atg atg aac	2187
Ser Leu Ala Ser Glu Tyr Ser Ile Pro Val Phe Asp Asn Met Met Asn	
355 360 365	
agg cac ctg gtg gcc caa gac ctg ttc tcg gtt tac atg gac agg aat	2235
Arg His Leu Val Ala Gln Asp Leu Phe Ser Val Tyr Met Asp Arg Asn	
370 375 380	
ggc cag gag agc atg ctc acg ctg ggg gcc atc gac ccg tcc tac tac	2283
Gly Gln Glu Ser Met Leu Thr Leu Gly Ala Ile Asp Pro Ser Tyr Tyr	
385 390 395	
aca ggg tcc ctg cac tgg gtg ccc gtg aca gtg cag cag tac tgg cag	2331
Thr Gly Ser Leu His Trp Val Pro Val Thr Val Gln Gln Tyr Trp Gln	
400 405 410	
ttc act gtg gac agt gtc acc atc agc ggt gtg gtt gtg gcc tgt gag	2379
Phe Thr Val Asp Ser Val Thr Ile Ser Gly Val Val Val Ala Cys Glu	
415 420 425 430	
ggt ggc tgt cag gcc atc ttg gac acg ggc acc tcc aag ctg gtc ggg	2427
Gly Gly Cys Gln Ala Ile Leu Asp Thr Gly Thr Ser Lys Leu Val Gly	
435 440 445	


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ccc agc agc gac atc ctc aac atc cag cag gcc att gga gcc aca cag 2475
Pro Ser Ser Asp Ile Leu Asn Ile Gln Gln Ala Ile Gly Ala Thr Gln
      450                      455                      460

aac cag tac ggt gag ttt gac atc gac tgc gac aac ctg agc tac atg 2523
Asn Gln Tyr Gly Glu Phe Asp Ile Asp Cys Asp Asn Leu Ser Tyr Met
      465                      470                      475

ccc act gtg gtc ttt gag atc aat ggc aaa atg tac cca ctg acc ccc 2571
Pro Thr Val Val Phe Glu Ile Asn Gly Lys Met Tyr Pro Leu Thr Pro
      480                      485                      490

tcc gcc tat acc agc caa gac cag ggc ttc tgt acc agt ggc ttc cag 2619
Ser Ala Tyr Thr Ser Gln Asp Gln Gly Phe Cys Thr Ser Gly Phe Gln
      495                      500                      505                      510

agt gaa aat cat tcc cag aaa tgg atc ctg ggg gat gtt ttc atc cga 2667
Ser Glu Asn His Ser Gln Lys Trp Ile Leu Gly Asp Val Phe Ile Arg
      515                      520                      525

gag tat tac agc gtc ttt gac agg gcc aac aac ctc gtg ggg ctg gcc 2715
Glu Tyr Tyr Ser Val Phe Asp Arg Ala Asn Asn Leu Val Gly Leu Ala
      530                      535                      540

aaa gcc atc tgaaagctt 2733
Lys Ala Ile
      545

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<210> 7

<211> 118

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Fragment of
pSBSOTPTNT containing the oleosin-chymosin fusion
gene

<400> 7

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Gln Tyr Pro Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met Ser Gly
      20                      25                      30

Arg Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr
      35                      40                      45

Ala Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu
      50                      55                      60

Val Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile
      65                      70                      75                      80

Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile
      85                      90                      95

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Thr Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val
 100 105 110

Phe Ser Trp Ile Tyr Lys
 115

<210> 8

<211> 427

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fragment of
 pSBSOTPTNT containing the oleosin-chymosin fusion
 gene

<400> 8

Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp Lys Leu Asp Ser Ala
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Arg Met Lys Leu Gly Ser Lys Ala Gln Asp Leu Lys Asp Arg Ala Gln
 20 25 30

Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp Arg Asp Arg Thr
 35 40 45

Arg Gly Gly Gln His Thr Thr Leu Val Pro Arg Gly Ser Met Ala Glu
 50 55 60

Ile Thr Arg Ile Pro Leu Tyr Lys Gly Lys Ser Leu Arg Lys Ala Leu
 65 70 75 80

Lys Glu His Gly Leu Leu Glu Asp Phe Leu Gln Lys Gln Gln Tyr Gly
 85 90 95

Ile Ser Ser Lys Tyr Ser Gly Phe Gly Glu Val Ala Ser Val Pro Leu
 100 105 110

Thr Asn Tyr Leu Asp Ser Gln Tyr Phe Gly Lys Ile Tyr Leu Gly Thr
 115 120 125

Pro Pro Gln Glu Phe Thr Val Leu Phe Asp Thr Gly Ser Ser Asp Phe
 130 135 140

Trp Val Pro Ser Ile Tyr Cys Lys Ser Asn Ala Cys Lys Asn His Gln
 145 150 155 160

Arg Phe Asp Pro Arg Lys Ser Ser Thr Phe Gln Asn Leu Gly Lys Pro
 165 170 175

Leu Ser Ile His Tyr Gly Thr Gly Ser Met Gln Gly Ile Leu Gly Tyr
 180 185 190

Asp Thr Val Thr Val Ser Asn Ile Val Asp Ile Gln Gln Thr Val Gly
 195 200 205

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Leu Ser Thr Gln Glu Pro Gly Asp Val Phe Thr Tyr Ala Glu Phe Asp
 210                               215                220

Gly Ile Leu Gly Met Ala Tyr Pro Ser Leu Ala Ser Glu Tyr Ser Ile
225                               230                235                240

Pro Val Phe Asp Asn Met Met Asn Arg His Leu Val Ala Gln Asp Leu
                               245                250                255

Phe Ser Val Tyr Met Asp Arg Asn Gly Gln Glu Ser Met Leu Thr Leu
                               260                265                270

Gly Ala Ile Asp Pro Ser Tyr Tyr Thr Gly Ser Leu His Trp Val Pro
 275                               280                285

Val Thr Val Gln Gln Tyr Trp Gln Phe Thr Val Asp Ser Val Thr Ile
 290                               295                300

Ser Gly Val Val Val Ala Cys Glu Gly Gly Cys Gln Ala Ile Leu Asp
305                               310                315                320

Thr Gly Thr Ser Lys Leu Val Gly Pro Ser Ser Asp Ile Leu Asn Ile
                               325                330                335

Gln Gln Ala Ile Gly Ala Thr Gln Asn Gln Tyr Gly Glu Phe Asp Ile
 340                               345                350

Asp Cys Asp Asn Leu Ser Tyr Met Pro Thr Val Val Phe Glu Ile Asn
 355                               360                365

Gly Lys Met Tyr Pro Leu Thr Pro Ser Ala Tyr Thr Ser Gln Asp Gln
 370                               375                380

Gly Phe Cys Thr Ser Gly Phe Gln Ser Glu Asn His Ser Gln Lys Trp
385                               390                395                400

Ile Leu Gly Asp Val Phe Ile Arg Glu Tyr Tyr Ser Val Phe Asp Arg
 405                               410                415

Ala Asn Asn Leu Val Gly Leu Ala Lys Ala Ile
 420                               425

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<210> 9

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 9

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Leu Val Pro Arg Gly
 1                5

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<210> 10
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 10
 Phe Glu Gly Arg
 1

<210> 11
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 11
 Pro Leu Gly Pro
 1

<210> 12
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 12
 Glu Asn Leu Tyr Phe Gln Gly
 1 5

<210> 13
 <211> 14
 <212> DNA
 <213> Daucus carota

<400> 13
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14

<210> 14
 <211> 14
 <212> DNA
 <213> Zea mays

<400> 14
 gcggtaacga cggc

14

<210> 15
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

<400> 15
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<210> 16
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

<400> 16
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<210> 17
 <211> 62
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

<400> 17
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 tc 62

<210> 18
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

<400> 18
 cactgcagga actctctggt aagc 24

<210> 19
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 19
 gaggatccat ggtacgctcct gtagaaacc

29

<210> 20
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 20
 gtaaaacgac ggccagt

17

<210> 21
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oleosin/GUS fusion protein

<400> 21
 Leu Val Pro Arg Gly Ser
 1 5

<210> 22
 <211> 9
 <212> PRT
 <213> Homo sapiens

<400> 22
 Val Gln Gly Glu Glu Ser Asn Asp Lys
 1 5

<210> 23
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 23
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28

<210> 24
 <211> 28

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 24
 cgcatcgatg ttcttggtta ctagagag

28

<210> 25
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 25
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36

<210> 26
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 26
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37

<210> 27
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 27
 cgcggatcca tggcggatac agctaga

27

<210> 28
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 28
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36

<210> 29
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 spacer sequence

<400> 29
 Leu Val Pro Arg Gly Ser
 1 5

<210> 30
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 30
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<210> 31
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 31
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<210> 32
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 32
 taccatggct tcggaagaag ga 22

<210> 33
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 33
gaaagcttaa gccaaagtgtt tg 22

<210> 34
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 34
ggccagcaca ctaccatgaa tggctctgaa actcac 36

<210> 35
<211> 28
<212> DNA
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<223> Description of Artificial Sequence: Primer

<400> 35
ttaagcttca atcactctta ccttgctg 28

<210> 36
<211> 1002
<212> DNA
<213> Unknown Organism

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<223> Description of Unknown Organism: Published NADPH
thioredoxin reductase sequence

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<221> CDS
<222> (1)..(999)

<400> 36
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ggc cca gcg gca cac acg gcg gcg att tac gca gct agg gct gaa ctt 96
Gly Pro Ala Ala His Thr Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu
20 25 30
aaa cct ctt ctc ttc gaa gga tgg atg gct aac gac atc gct ccc ggt 144
Lys Pro Leu Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala Pro Gly
35 40 45
ggt caa cta aca acc acc acc gac gtc gag aat ttc ccc gga ttt cca 192
Gly Gln Leu Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Pro
50 55 60

gaa ggt att ctc gga gta gag ctc act gac aaa ttc cgt aaa caa tcg	240
Glu Gly Ile Leu Gly Val Glu Leu Thr Asp Lys Phe Arg Lys Gln Ser	
65 70 75 80	
gag cga ttc ggt act acg ata ttt aca gag acg gtg acg aaa gtc gat	288
Glu Arg Phe Gly Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp	
85 90 95	
ttc tct tcg aaa ccg ttt aag cta ttc aca gat tca aaa gcc att ctc	336
Phe Ser Ser Lys Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu	
100 105 110	
gct gac gct gtg att ctc gct act gga gct gtg gct aag cgg ctt agc	384
Ala Asp Ala Val Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser	
115 120 125	
ttc gtt gga tct ggt gaa ggt tct gga ggt ttc tgg aac cgt gga atc	432
Phe Val Gly Ser Gly Glu Gly Ser Gly Gly Phe Trp Asn Arg Gly Ile	
130 135 140	
tcc gct tgt gct gtt tgc gac gga gct gct ccg ata ttc cgt aac aaa	480
Ser Ala Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys	
145 150 155 160	
cct ctt gcg gtg atc ggt gga ggc gat tca gca atg gaa gaa gca aac	528
Pro Leu Ala Val Ile Gly Gly Gly Asp Ser Ala Met Glu Glu Ala Asn	
165 170 175	
ttt ctt aca aaa tat gga tct aaa gtg tat ata atc cat agg aga gat	576
Phe Leu Thr Lys Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp	
180 185 190	
gct ttt aga gcg tct aag att atg cag cag cga gct ttg tct aat cct	624
Ala Phe Arg Ala Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro	
195 200 205	
aag att gat gtg att tgg aac tcg tct gtt gtg gaa gct tat gga gat	672
Lys Ile Asp Val Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp	
210 215 220	
gga gaa aga gat gtg ctt gga gga ttg aaa gtg aag aat gtg gtt acc	720
Gly Glu Arg Asp Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr	
225 230 235 240	
gga gat gtt tct gat tta aaa gtt tct gga ttg ttc ttt gct att ggt	768
Gly Asp Val Ser Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly	
245 250 255	
cat gag cca gct acc aag ttt ttg gat ggt ggt gtt gag tta gat tcg	816
His Glu Pro Ala Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser	
260 265 270	
gat ggt tat gtt gtc acg aag cct ggt act aca cag act agc gtt ccc	864
Asp Gly Tyr Val Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro	
275 280 285	

gga gtt ttc gct gcg ggt gat gtt cag gat aag aag tat agg caa gcc 912
 Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala
 290 295 300

atc act gct gca gga act ggg tgc atg gca gct ttg gat gca gag cat 960
 Ile Thr Ala Ala Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His
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 Tyr Leu Gln Glu Ile Gly Ser Gln Gln Gly Lys Ser Asp
 325 330

<210> 37
 <211> 1002
 <212> DNA
 <213> Arabidopsis sp.

<220>
 <221> CDS
 <222> (1)..(999)

<400> 37

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ggc cca gcg gca cac acg gcg gcg att tac gca gct agg gct gaa ctt 96
 Gly Pro Ala Ala His Thr Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu
 20 25 30

aaa cct ctt ctc ttc gaa gga tgg atg gct aac gac atc gct ccc ggt 144
 Lys Pro Leu Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala Pro Gly
 35 40 45

ggt caa cta aca acc acc acc gac gtc gag aat ttc ccc gga ttt cca 192
 Gly Gln Leu Thr Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Pro
 50 55 60

gaa ggt att ctc gga gta gag ctc act gac aaa ttc cgt aaa caa tcg 240
 Glu Gly Ile Leu Gly Val Glu Leu Thr Asp Lys Phe Arg Lys Gln Ser
 65 70 75 80

gag cga ttc ggt act acg ata ttt aca gag acg gtg acg aaa gtc gat 288
 Glu Arg Phe Gly Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp
 85 90 95

ttc tct tcg aaa ccg ttt aag cta ttc aca gat tca aaa gcc att ctc 336
 Phe Ser Ser Lys Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu
 100 105 110

gct gac gct gtg att ctc gct act gga gct gtg gct aag cgg ctt agc 384
 Ala Asp Ala Val Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser
 115 120 125

ttc gtt gga tct ggt gaa ggt tct gga ggt ttc tgg aac cgt gga atc 432
 Phe Val Gly Ser Gly Glu Gly Ser Gly Gly Phe Trp Asn Arg Gly Ile
 130 135 140

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tcc gct tgt gct gtt tgc gac gga gct gct ccg ata ttc cgt aac aaa 480
Ser Ala Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys
145                      150                      155                      160

cct ctt gcg gtg atc ggt gga ggc gat tca gca atg gaa gaa gca aac 528
Pro Leu Ala Val Ile Gly Gly Gly Asp Ser Ala Met Glu Glu Ala Asn
165                      170                      175

ttt ctt aca aaa tat gga tct aaa gtg tat ata atc cat agg aga gat 576
Phe Leu Thr Lys Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp
180                      185                      190

gct ttt aga gcg tct aag att atg cag cag cga gct ttg tct aat cct 624
Ala Phe Arg Ala Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro
195                      200                      205

aag att gat gtg att tgg aac tcg tct gtt gtg gaa gct tat gga gat 672
Lys Ile Asp Val Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp
210                      215                      220

gga gaa aga gat gtg ctt gga gga ttg aaa gtg aag aat gtg gtt acc 720
Gly Glu Arg Asp Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr
225                      230                      235                      240

gga gat gtt tct gat tta aaa gtt tct gga ttg ttc ttt gct att ggt 768
Gly Asp Val Ser Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly
245                      250                      255

cat gag cca gct acc aag ttt ttg gat ggt ggt gtt gag tta gat tcg 816
His Glu Pro Ala Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser
260                      265                      270

gat ggt tat gtt gtc acg aag cct ggt act aca cag act agc gtt ccc 864
Asp Gly Tyr Val Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro
275                      280                      285

gga gtt ttc gct gcg ggt gat gtt cag gat aag aag tat agg caa gcc 912
Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala
290                      295                      300

atc act gct gca gga act ggg tgc atg gca gct ttg gat gca gag cat 960
Ile Thr Ala Ala Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His
305                      310                      315                      320

tac tta caa gag att gga tct cag caa ggt aag agt gat tga 1002
Tyr Leu Gln Glu Ile Gly Ser Gln Gln Gly Lys Ser Asp
325                      330

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<210> 38

<211> 333

<212> PRT

<213> Arabidopsis sp.

<400> 38

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Met Asn Gly Leu Glu Thr His Asn Thr Arg Leu Cys Ile Val Gly Ser
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Lys	Pro	Leu	Leu	Phe	Glu	Gly	Trp	Met	Ala	Asn	Asp	Ile	Ala	Pro	Gly	35	40	45	
Gly	Gln	Leu	Thr	Thr	Thr	Thr	Asp	Val	Glu	Asn	Phe	Pro	Gly	Phe	Pro	50	55	60	
Glu	Gly	Ile	Leu	Gly	Val	Glu	Leu	Thr	Asp	Lys	Phe	Arg	Lys	Gln	Ser	65	70	75	80
Glu	Arg	Phe	Gly	Thr	Thr	Ile	Phe	Thr	Glu	Thr	Val	Thr	Lys	Val	Asp	85	90	95	
Phe	Ser	Ser	Lys	Pro	Phe	Lys	Leu	Phe	Thr	Asp	Ser	Lys	Ala	Ile	Leu	100	105	110	
Ala	Asp	Ala	Val	Ile	Leu	Ala	Thr	Gly	Ala	Val	Ala	Lys	Arg	Leu	Ser	115	120	125	
Phe	Val	Gly	Ser	Gly	Glu	Gly	Ser	Gly	Gly	Phe	Trp	Asn	Arg	Gly	Ile	130	135	140	
Ser	Ala	Cys	Ala	Val	Cys	Asp	Gly	Ala	Ala	Pro	Ile	Phe	Arg	Asn	Lys	145	150	155	160
Pro	Leu	Ala	Val	Ile	Gly	Gly	Gly	Asp	Ser	Ala	Met	Glu	Glu	Ala	Asn	165	170	175	
Phe	Leu	Thr	Lys	Tyr	Gly	Ser	Lys	Val	Tyr	Ile	Ile	His	Arg	Arg	Asp	180	185	190	
Ala	Phe	Arg	Ala	Ser	Lys	Ile	Met	Gln	Gln	Arg	Ala	Leu	Ser	Asn	Pro	195	200	205	
Lys	Ile	Asp	Val	Ile	Trp	Asn	Ser	Ser	Val	Val	Glu	Ala	Tyr	Gly	Asp	210	215	220	
Gly	Glu	Arg	Asp	Val	Leu	Gly	Gly	Leu	Lys	Val	Lys	Asn	Val	Val	Thr	225	230	235	240
Gly	Asp	Val	Ser	Asp	Leu	Lys	Val	Ser	Gly	Leu	Phe	Phe	Ala	Ile	Gly	245	250	255	
His	Glu	Pro	Ala	Thr	Lys	Phe	Leu	Asp	Gly	Gly	Val	Glu	Leu	Asp	Ser	260	265	270	
Asp	Gly	Tyr	Val	Val	Thr	Lys	Pro	Gly	Thr	Thr	Gln	Thr	Ser	Val	Pro	275	280	285	
Gly	Val	Phe	Ala	Ala	Gly	Asp	Val	Gln	Asp	Lys	Lys	Tyr	Arg	Gln	Ala	290	295	300	
Ile	Thr	Ala	Ala	Gly	Thr	Gly	Cys	Met	Ala	Ala	Leu	Asp	Ala	Glu	His	305	310	315	320

Tyr Leu Gln Glu Ile Gly Ser Gln Gln Gly Lys Ser Asp
 325 330

<210> 39

<211> 333

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Published NADPH
 thioredoxin reductase sequence

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Gly Pro Ala Ala His Thr Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu
 20 25 30

Lys Pro Leu Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala Pro Gly
 35 40 45

Gly Gln Leu Thr Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Pro
 50 55 60

Glu Gly Ile Leu Gly Val Glu Leu Thr Asp Lys Phe Arg Lys Gln Ser
 65 70 75 80

Glu Arg Phe Gly Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp
 85 90 95

Phe Ser Ser Lys Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu
 100 105 110

Ala Asp Ala Val Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser
 115 120 125

Phe Val Gly Ser Gly Glu Gly Ser Gly Gly Phe Trp Asn Arg Gly Ile
 130 135 140

Ser Ala Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys
 145 150 155 160

Pro Leu Ala Val Ile Gly Gly Gly Asp Ser Ala Met Glu Glu Ala Asn
 165 170 175

Phe Leu Thr Lys Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp
 180 185 190

Ala Phe Arg Ala Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro
 195 200 205

Lys Ile Asp Val Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp
 210 215 220

Gly Glu Arg Asp Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr
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<221> CDS  
<222> (1555) .. (1896)
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tatccctaca	aattttattat	ttgttaaaca	ttttcaaacc	gcataaaaatt	ttatgaagtc	240	
ccgtctatct	ttaatgtagt	ctaacatttt	catattgaaa	tatataattt	acttaatttt	300	
agcgttggtg	gaaagcataa	tgattttattc	ttattcttct	tcatataaat	gtttaatatata	360	
caatataaac	aaattcttta	ccttaagaag	gatttcccat	tttatatttt	aaaaatatat	420	
ttatcaaata	tttttcaacc	acgtaaatct	cataataata	agttgtttca	aaagtaataa	480	
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ataattccca	tttgacacta	cggaagtaac	tgaagatctg	cttttacatg	cgagacacat	720	
cttctaaagt	aattttaata	atagttacta	tattcaagat	ttcatatatc	aaatactcaa	780	
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aattgttgaa tttgtgacta ttgatttatt attctactat gtttaaattg ttttatagat 900
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Asn Glu Gln Leu Gln Lys Ala Asn Glu Ser Lys Thr Leu Val Val Val
20 25 30
gat ttc acg gct tct tgg tgt gga cca tgt cgt ttc atc gct cca ttc 1701
Asp Phe Thr Ala Ser Trp Cys Gly Pro Cys Arg Phe Ile Ala Pro Phe
35 40 45
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Phe Ala Asp Leu Ala Lys Lys Leu Pro Asn Val Leu Phe Leu Lys Val
50 55 60 65
gat act gat gaa ttg aag tcg gtg gca agt gat tgg gcg ata cag gcg 1797
Asp Thr Asp Glu Leu Lys Ser Val Ala Ser Asp Trp Ala Ile Gln Ala
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atg cca acc ttc atg ttt ttg aag gaa ggg aag att ttg gac aaa gtt 1845
Met Pro Thr Phe Met Phe Leu Lys Glu Gly Lys Ile Leu Asp Lys Val
85 90 95
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Val Gly Ala Lys Lys Asp Glu Leu Gln Ser Thr Ile Ala Lys His Leu
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gct taagcttaat aagtatgaac taaaatgcat gtaggtgtaa gagctcatgg 1946
Ala
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<211> 114

<212> PRT

<213> *Arabidopsis thaliana*

<400> 41

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			20					25					30		
Val	Asp	Phe	Thr	Ala	Ser	Trp	Cys	Gly	Pro	Cys	Arg	Phe	Ile	Ala	Pro
		35					40					45			
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Val Asp Thr Asp Glu Leu Lys Ser Val Ala Ser Asp Trp Ala Ile Gln
 65 70 75 80

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Val Val Gly Ala Lys Lys Asp Glu Leu Gln Ser Thr Ile Ala Lys His
 100 105 110

Leu Ala

<210> 42
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<220>
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<220>
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 <222> (2149)..(2655)

<220>
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 promoter-oleosin Trxh-phaseolin terminator

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 tatccctaca aatttattat ttgttaaaca ttttcaaacc gcataaaatt ttatgaagtc 240
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 aatttaactc cataattttt ttattcgact gatcttaaag caacaccag tgacacaact 540
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Tyr Pro Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met Ser Gly Arg
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gga tct gac tac tcc aag tct agg cag att gct aaa gct gca act gct 1701
Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr Ala
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gtc aca gct ggt ggt tcc ctc ctt gtt ctc tcc agc ctt acc ctt gtt 1749
Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu Val
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Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile Phe
70 75 80
agc cca atc ctt gtc ccg gct ctc atc aca gtt gca ctc ctc atc acc 1845
Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile Thr
85 90 95
ggg ttt ctt tcc tct gga ggg ttt ggc att gcc gct ata acc gtt ttc 1893
Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val Phe
100 105 110
tct tgg att tac aag taagcacaca tttatcatct tacttcataa ttttgtgcaa 1948
Ser Trp Ile Tyr Lys
115

tatgtgcatg catgtgttga gccagtagct ttggatcaat ttttttggtc gaataacaaa 2008
 tgtaacaata agaaattgca aattctaggg aacatttggt taactaaata cgaaatttga 2068
 cctagctagc ttgaatgtgt ctgtgtatat catctatata ggtaaaatgc ttggtatgat 2128
 acctattgat tgtgaatagg tac gca acg gga gag cac cca cag gga tca gac 2181
 Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp
 120 125
 aag ttg gac agt gca agg atg aag ttg gga agc aaa gct cag gat ctg 2229
 Lys Leu Asp Ser Ala Arg Met Lys Leu Gly Ser Lys Ala Gln Asp Leu
 130 135 140 145
 aaa gac aga gct cag tac tac gga cag caa cat act ggt ggg gaa cat 2277
 Lys Asp Arg Ala Gln Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His
 150 155 160
 gac cgt gac cgt act cgt ggt ggc cag cac act acc atg gct tcg gaa 2325
 Asp Arg Asp Arg Thr Arg Gly Gly Gln His Thr Thr Met Ala Ser Glu
 165 170 175
 gaa gga caa gtg atc gcc tgc cac acc gtt gag aca tgg aac gag cag 2373
 Glu Gly Gln Val Ile Ala Cys His Thr Val Glu Thr Trp Asn Glu Gln
 180 185 190
 ctt cag aag gct aat gaa tcc aaa act ctt gtg gtg gtt gat ttc acg 2421
 Leu Gln Lys Ala Asn Glu Ser Lys Thr Leu Val Val Val Asp Phe Thr
 195 200 205
 gct tct tgg tgt gga cca tgt cgt ttc atc gct cca ttc ttt gct gat 2469
 Ala Ser Trp Cys Gly Pro Cys Arg Phe Ile Ala Pro Phe Phe Ala Asp
 210 215 220 225
 ttg gct aag aaa ctt cct aac gtg ctt ttc ctc aag gtt gat act gat 2517
 Leu Ala Lys Lys Leu Pro Asn Val Leu Phe Leu Lys Val Asp Thr Asp
 230 235 240
 gaa ttg aag tcg gtg gca agt gat tgg gcg ata cag gcg atg cca acc 2565
 Glu Leu Lys Ser Val Ala Ser Asp Trp Ala Ile Gln Ala Met Pro Thr
 245 250 255
 ttc atg ttt ttg aag gaa ggg aag att ttg gac aaa gtt gtt gga gcc 2613
 Phe Met Phe Leu Lys Glu Gly Lys Ile Leu Asp Lys Val Val Gly Ala
 260 265 270
 aag aaa gat gag ctt cag tct acc att gcc aaa cac ttg gct 2655
 Lys Lys Asp Glu Leu Gln Ser Thr Ile Ala Lys His Leu Ala
 275 280 285
 taagcttaat aagtatgaac taaaatgcat gtaggtgtaa gagctcatgg agagcatgga 2715
 atattgtatc cgaccatgta acagtataat aactgagctc catctcactt cttctatgaa 2775
 taaacaaagg atgttatgat atattaacac tctatctatg caccttattg ttctatgata 2835
 aatttcctct tattattata aatcatctga atcgtgacgg cttatggaat gttcaaata 2895

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gtacaaaaac aaatgtgtac tataagactt tctaaacaat tctaacttta gcattgtgaa 2955
cgagacataa gtgtaagaa gacataacaa ttataatgga agaagtttgt ctccatttat 3015
atattatata ttaccactt atgtattata ttaggatgtt aaggagacat aacaattata 3075
aagagagaag tttgtatcca tttatatatt atatactacc catttatata ttatacttat 3135
ccacttattt aatgtcttta taaggtttga tccatgatat ttctaataatt ttagttgata 3195
tgtatatgaa aggggtactat ttgaactctc ttactctgta taaaggttgg atcatcctta 3255
aagtgggtct atttaatttt attgcttctt acagataaaa aaaaaattat gagttggttt 3315
gataaaatat tgaaggattt aaaataataa taaataataa ataacatata atatatgtat 3375
ataaatttat tataatataa catttatcta taaaaaagta aatattgtca taaatctata 3435
caatcgttta gccttgctgg acgactctca attatttaa cgagagtaaa catatttgac 3495
tttttggtta ttttaacaaat tattatttaa cactatatga aatttttttt ttttatcggc 3555
aaggaaataa aattaaatta ggagggacaa tgggtgtgtcc caatccttat acaaccaact 3615
tccacaggaa ggtcaggctg gggacaacaa aaaaacaggc aagggaatt ttttaatttg 3675
ggttgtcttg tttgctgcat aatttatgca gtaaaacact acacataacc cttttagcag 3735
tagagcaatg gttgaccgtg tgcttagctt cttttatttt atttttttat cagcaaagaa 3795
taaataaaat aaaatgagac acttcagga tgtttcaacc cttatacaaa accccaaaaa 3855
caagtttcct agcaccctac caactaaggt acc 3888

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<210> 43

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Phaseolin
promoter-oleosin Trxh-phaseolin terminator

<400> 43

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Met Ala Asp Thr Ala Arg Gly Thr His His Asp Ile Ile Gly Arg Asp
  1             5             10             15

```

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Gln Tyr Pro Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met Ser Gly
          20             25             30

```

```

Arg Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr
      35             40             45

```

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Ala Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu
      50             55             60

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Val Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile
65 70 75 80

Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile
85 90 95

Thr Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val
100 105 110

Phe Ser Trp Ile Tyr Lys
115

<210> 44
<211> 169
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Phaseolin
promoter-oleosin Trxh-phaseolin terminator

<400> 44
Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp Lys Leu Asp Ser Ala
1 5 10 15

Arg Met Lys Leu Gly Ser Lys Ala Gln Asp Leu Lys Asp Arg Ala Gln
20 25 30

Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp Arg Asp Arg Thr
35 40 45

Arg Gly Gly Gln His Thr Thr Met Ala Ser Glu Glu Gly Gln Val Ile
50 55 60

Ala Cys His Thr Val Glu Thr Trp Asn Glu Gln Leu Gln Lys Ala Asn
65 70 75 80

Glu Ser Lys Thr Leu Val Val Val Asp Phe Thr Ala Ser Trp Cys Gly
85 90 95

Pro Cys Arg Phe Ile Ala Pro Phe Phe Ala Asp Leu Ala Lys Lys Leu
100 105 110

Pro Asn Val Leu Phe Leu Lys Val Asp Thr Asp Glu Leu Lys Ser Val
115 120 125

Ala Ser Asp Trp Ala Ile Gln Ala Met Pro Thr Phe Met Phe Leu Lys
130 135 140

Glu Gly Lys Ile Leu Asp Lys Val Val Gly Ala Lys Lys Asp Glu Leu
145 150 155 160

Gln Ser Thr Ile Ala Lys His Leu Ala
165

<210> 45
 <211> 3888
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Phaseolin
 promoter-Trxh oleosin-phaseolin terminator

<220>
 <221> CDS
 <222> (1555)..(2250)

<220>
 <221> CDS
 <222> (2491)..(2655)

<400> 45
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 tggtttttta cctctattta aaggggtttt ccacctaaaa attctggtat cattctcact 120
 ttacttggtta ctttaatttc tcataatctt tggttgaaat tatcacgctt ccgcacacga 180
 tatccctaca aatttattat ttgttaaaca ttttcaaacc gcataaaatt ttatgaagtc 240
 ccgtctatct ttaatgtagt ctaacatctt catattgaaa tatataattt acttaatttt 300
 agcgttggtg gaaagcataa tgattttatc ttattcttct tcatataaat gtttaataata 360
 caatataaac aaattcttta ccttaagaag gatttcccat tttatatttt aaaaatatat 420
 ttatcaaata tttttcaacc acgtaaatct cataataata agttgtttca aaagtaataa 480
 aatttaactc cataattttt ttattcgact gatcttaaag caacaccag tgacacaact 540
 agccattttt ttctttgaat aaaaaaatcc aattatcatt gtattttttt tatacaatga 600
 aaatttcacc aaacaatcat ttgtggtatt tctgaagcaa gtcattgttat gcaaaattct 660
 ataattccca ttgacacta cggaagtaac tgaagatctg cttttacatg cgagacacat 720
 cttctaaagt aattttaata atagttacta tattcaagat ttcatatatc aaataactca 780
 tattacttct aaaaaattaa ttagatataa ttaaaatatt acttttttaa ttttaagttt 840
 aattggtgaa tttgtgacta ttgatttatt attctactat gtttaaattg ttttatagat 900
 agtttaagat aaatataagt aatgtagtag agtgtagtag tgttacccta aaccataaac 960
 tataagattt atggtggact aattttcata tatttcttat tgcttttacc ttttcttggg 1020
 atgtaagtcc gtaactggaa ttactgtggg ttgccatggc actctgtggg cttttgggtc 1080
 atgcatggat gcttgcgcaa gaaaaagaca aagaacaaag aaaaaagaca aaacagagag 1140
 acaaacgca atcacacaac caactcaaat tagtcactgg ctgatcaaga tcgccgcgctc 1200

catgtatgtc taaatgccat gcaaagcaac acgtgcttaa catgcacttt aaatggctca 1260
cccatctcaa cccacacaca aacacattgc cttttttcttc atcatcacca caaccacctg 1320
tatatatcca ttctcttccg ccacctcaat ttcttcaact caacacacgt caacctgcat 1380
atgcgtgtca tcccatgccc aaatctccat gcatgttcca accaccttct ctcttatata 1440
atacctataa atacctctaa tatcactcac ttcttttcac atccatccat ccagagtact 1500
actactctac tactataata ccccaaccca actcatattc aatactactc tact atg 1557
Met
1
gct tcg gaa gaa gga caa gtg atc gcc tgc cac acc gtt gag aca tgg 1605
Ala Ser Glu Glu Gly Gln Val Ile Ala Cys His Thr Val Glu Thr Trp
5 10 15
aac gag cag ctt cag aag gct aat gaa tcc aaa act ctt gtg gtg gtt 1653
Asn Glu Gln Leu Gln Lys Ala Asn Glu Ser Lys Thr Leu Val Val Val
20 25 30
gat ttc acg gct tct tgg tgt gga cca tgt cgt ttc atc gct cca ttc 1701
Asp Phe Thr Ala Ser Trp Cys Gly Pro Cys Arg Phe Ile Ala Pro Phe
35 40 45
ttt gct gat ttg gct aag aaa ctt cct aac gtg ctt ttc ctc aag gtt 1749
Phe Ala Asp Leu Ala Lys Lys Leu Pro Asn Val Leu Phe Leu Lys Val
50 55 60 65
gat act gat gaa ttg aag tcg gtg gca agt gat tgg gcg ata cag gcg 1797
Asp Thr Asp Glu Leu Lys Ser Val Ala Ser Asp Trp Ala Ile Gln Ala
70 75 80
atg cca acc ttc atg ttt ttg aag gaa ggg aag att ttg gac aaa gtt 1845
Met Pro Thr Phe Met Phe Leu Lys Glu Gly Lys Ile Leu Asp Lys Val
85 90 95
gtt gga gcc aag aaa gat gag ctt cag tct acc att gcc aaa cac ttg 1893
Val Gly Ala Lys Lys Asp Glu Leu Gln Ser Thr Ile Ala Lys His Leu
100 105 110
gct atg gcg gat aca gct aga gga acc cat cac gat atc atc ggc aga 1941
Ala Met Ala Asp Thr Ala Arg Gly Thr His His Asp Ile Ile Gly Arg
115 120 125
gac cag tac ccg atg atg ggc cga gac cga gac cag tac cag atg tcc 1989
Asp Gln Tyr Pro Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met Ser
130 135 140 145
gga cga gga tct gac tac tcc aag tct agg cag att gct aaa gct gca 2037
Gly Arg Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala
150 155 160
act gct gtc aca gct ggt ggt tcc ctc ctt gtt ctc tcc agc ctt acc 2085
Thr Ala Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr
165 170 175

ctt gtt gga act gtc ata gct ttg act gtt gca aca cct ctg ctc gtt 2133
 Leu Val Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val
 180 185 190

atc ttc agc cca atc ctt gtc ccg gct ctc atc aca gtt gca ctc ctc 2181
 Ile Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu
 195 200 205

atc acc ggt ttt ctt tcc tct gga ggg ttt ggc att gcc gct ata acc 2229
 Ile Thr Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr
 210 215 220 225

gtt ttc tct tgg att tac aag taagcacaca tttatcatct tacttcataa 2280
 Val Phe Ser Trp Ile Tyr Lys
 230

ttttgtgcaa tatgtgcatg catgtgttga gccagtagct ttggatcaat ttttttggtc 2340

gaataacaaa tgtaacaata agaaattgca aattctaggg aacatttggt taactaaata 2400

cgaaatttga cctagctagc ttgaatgtgt ctgtgtatat catctatata ggtaaaatgc 2460

ttggatatgat acctattgat tgtgaatagg tac gca acg gga gag cac cca cag 2514
 Tyr Ala Thr Gly Glu His Pro Gln
 235 240

gga tca gac aag ttg gac agt gca agg atg aag ttg gga agc aaa gct 2562
 Gly Ser Asp Lys Leu Asp Ser Ala Arg Met Lys Leu Gly Ser Lys Ala
 245 250 255

cag gat ctg aaa gac aga gct cag tac tac gga cag caa cat act ggt 2610
 Gln Asp Leu Lys Asp Arg Ala Gln Tyr Tyr Gly Gln Gln His Thr Gly
 260 265 270

ggg gaa cat gac cgt gac cgt act cgt ggt ggc cag cac act act 2655
 Gly Glu His Asp Arg Asp Arg Thr Arg Gly Gly Gln His Thr Thr
 275 280 285

taagcttaat aagtatgaac taaaatgcat gtaggtgtaa gagctcatgg agagcatgga 2715

atattgtatc cgaccatgta acagtataat aactgagctc catctcactt cttctatgaa 2775

taaacaaagg atgttatgat atattaacac tctatctatg caccttattg ttctatgata 2835

aatttcctct tattattata aatcatctga atcgtgacgg cttatggaat gcttcaaata 2895

gtacaaaaac aaatgtgtac tataagactt tctaaacaat tctaacttta gcattgtgaa 2955

cgagacataa gtgttaagaa gacataacaa ttataatgga agaagtttgt ctccatttat 3015

atattatata ttaccactt atgtattata ttaggatgtt aaggagacat aacaattata 3075

aagagagaag tttgtatcca tttatatatt atatactacc catttatata ttatacttat 3135

ccacttatctt aatgtcttta taaggtttga tccatgatat ttctaattatt ttagttgata 3195

tgtatatgaa agggacttat ttgaactctc ttactctgta taaaggttgg atcatcctta 3255

aagtgggtct atttaatttt attgcttctt acagataaaa aaaaaattat gagttgggtt 3315
gataaaatat tgaaggattt aaaataataa taaataataa ataacatata atatatgtat 3375
ataaattttat tataatataa catttatcta taaaaaagta aatattgtca taaatctata 3435
caatcgttta gccttgctgg acgactctca attattttaa cgagagtaaa catatttgac 3495
tttttggtta ttttaacaaat tattatttaa cactatatga aatttttttt ttttatcggc 3555
aaggaaataa aattaaatta ggagggacaa tgggtgtgtcc caatccttat acaaccaact 3615
tccacaggaa ggtcaggctg gggacaacaa aaaaacaggc aagggaattt ttttaatttg 3675
ggttgtcttg tttgctgcat aatttatgca gtaaaacact acacataacc cttttagcag 3735
tagagcaatg gttgaccgtg tgcttagctt cttttatttt atttttttat cagcaaagaa 3795
taaataaaat aaaatgagac acttcaggga tgtttcaacc cttatacaaa accccaaaaa 3855
caagtttcct agcaccctac caactaaggt acc 3888

<210> 46

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Phaseolin
promoter-Trxh oleosin-phaseolin terminator

<400> 46

Met	Ala	Ser	Glu	Gly	Gln	Val	Ile	Ala	Cys	His	Thr	Val	Glu	Thr
1				5				10					15	
Trp	Asn	Glu	Gln	Leu	Gln	Lys	Ala	Asn	Glu	Ser	Lys	Thr	Leu	Val
			20					25					30	Val
Val	Asp	Phe	Thr	Ala	Ser	Trp	Cys	Gly	Pro	Cys	Arg	Phe	Ile	Ala
			35					40					45	Pro
Phe	Phe	Ala	Asp	Leu	Ala	Lys	Lys	Leu	Pro	Asn	Val	Leu	Phe	Leu
			50				55				60			Lys
Val	Asp	Thr	Asp	Glu	Leu	Lys	Ser	Val	Ala	Ser	Asp	Trp	Ala	Ile
			65			70				75				80
Ala	Met	Pro	Thr	Phe	Met	Phe	Leu	Lys	Glu	Gly	Lys	Ile	Leu	Asp
				85					90					95
Val	Val	Gly	Ala	Lys	Lys	Asp	Glu	Leu	Gln	Ser	Thr	Ile	Ala	Lys
			100					105					110	His
Leu	Ala	Met	Ala	Asp	Thr	Ala	Arg	Gly	Thr	His	His	Asp	Ile	Ile
			115				120					125		Gly

Arg Asp Gln Tyr Pro Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met
 130 135 140
 Ser Gly Arg Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala
 145 150 155 160
 Ala Thr Ala Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu
 165 170 175
 Thr Leu Val Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu
 180 185 190
 Val Ile Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu
 195 200 205
 Leu Ile Thr Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile
 210 215 220
 Thr Val Phe Ser Trp Ile Tyr Lys
 225 230

<210> 47
 <211> 55
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Phaseolin
 promoter-Trxh oleosin-phaseolin terminator

<400> 47
 Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp Lys Leu Asp Ser Ala
 1 5 10 15
 Arg Met Lys Leu Gly Ser Lys Ala Gln Asp Leu Lys Asp Arg Ala Gln
 20 25 30
 Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp Arg Asp Arg Thr
 35 40 45
 Arg Gly Gly Gln His Thr Thr
 50 55

<210> 48
 <211> 3787
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Phaseolin
 promoter-thioredoxin reductase-phaseolin
 terminator

<220>
 <221> CDS
 <222> (1555) .. (2553)

<400> 48
 ctgcaggaat tcattgtact cccagtatca ttatagtga agttttggct ctctcgccgg 60
 tggtttttta cctctattta aaggggtttt ccacctaaaa attctggtat cattctcact 120
 ttacttggtta ctttaatttc tcataatctt tgggtgaaat tatcacgctt ccgcacacga 180
 tatccctaca aatttattat ttgttaaaca ttttcaaacc gcataaaatt ttatgaagtc 240
 ccgtctatct ttaatgtagt ctaacatttt catattgaaa tatataattt acttaatttt 300
 agcgttggtta gaaagcataa tgatttattc ttattcttct tcatataaat gtttaataata 360
 caatataaac aaattcttta ccttaagaag gatttcccat tttatatttt aaaaatatat 420
 ttatcaaata tttttcaacc acgtaaatct cataataata agttgtttca aaagtaataa 480
 aatttaactc cataattttt ttattcgact gatcttaaag caacaccag tgacacaact 540
 agccattttt ttctttgaat aaaaaaatcc aattatcatt gtattttttt tatacaatga 600
 aaatttcacc aaacaatcat ttgtggtatt tctgaagcaa gtcattgtat gcaaaattct 660
 ataattcca tttgacacta cggaagtaac tgaagatctg cttttacatg cgagacacat 720
 cttctaaagt aattttaata atagttacta tattcaagat ttcatatatc aaatactcaa 780
 tattacttct aaaaaattaa ttagatataa ttaaaatatt acttttttaa ttttaagttt 840
 aattgttgaa tttgtgacta ttgatttatt attctactat gtttaaattg ttttatagat 900
 agtttaaagt aaatataagt aatgtagtag agtggttagag tgttacccta aaccataaac 960
 tataagattt atggtggact aattttcata tatttcttat tgcttttacc ttttcttggt 1020
 atgtaagtcc gtaactggaa ttactgtggg ttgccatggc actctgtggt cttttggttc 1080
 atgcatggat gcttgcgcaa gaaaaagaca aagaacaaag aaaaagaca aaacagagag 1140
 aaaaaacgca atcacacaac caactcaaat tagtcaactgg ctgatcaaga tcgccgcgtc 1200
 catgtatgtc taaatgccat gcaaagcaac acgtgcttaa catgcacttt aaatgggtca 1260
 cccatctcaa cccacacaca aacacattgc ctttttcttc atcatcacca caaccacctg 1320
 tatatattca ttctcttcg ccacctcaat ttcttcactt caacacacgt caacctgcat 1380
 atgcgtgtca tcccatgccc aaatctccat gcatgttcca accaccttct ctcttatata 1440
 atacctataa atacctctaa tatcactcac ttctttcatt atccatccat ccagagtact 1500
 actactctac tactataata cccaacca actcatatcc aatactactc tact atg 1557
 Met
 1

aat ggt ctc gaa act cac aac aca agg ctc tgt atc gta gga agt ggc	1605
Asn Gly Leu Glu Thr His Asn Thr Arg Leu Cys Ile Val Gly Ser Gly	
5 10 15	
cca gcg gca cac acg gcg gcg att tac gca gct agg gct gaa ctt aaa	1653
Pro Ala Ala His Thr Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu Lys	
20 25 30	
cct ctt ctc ttc gaa gga tgg atg gct aac gac atc gct ccc ggt ggt	1701
Pro Leu Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala Pro Gly Gly	
35 40 45	
caa cta aca acc acc acc gac gtc gag aat ttc ccc gga ttt cca gaa	1749
Gln Leu Thr Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Pro Glu	
50 55 60 65	
ggt att ctc gga gta gag ctc act gac aaa ttc cgt aaa caa tcg gag	1797
Gly Ile Leu Gly Val Glu Leu Thr Asp Lys Phe Arg Lys Gln Ser Glu	
70 75 80	
cga ttc ggt act acg ata ttt aca gag acg gtg acg aaa gtc gat ttc	1845
Arg Phe Gly Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp Phe	
85 90 95	
tct tcg aaa ccg ttt aag cta ttc aca gat tca aaa gcc att ctc gct	1893
Ser Ser Lys Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu Ala	
100 105 110	
gac gct gtg att ctc gct act gga gct gtg gct aag cgg ctt agc ttc	1941
Asp Ala Val Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser Phe	
115 120 125	
gtt gga tct ggt gaa ggt tct gga ggt ttc tgg aac cgt gga atc tcc	1989
Val Gly Ser Gly Glu Gly Ser Gly Gly Phe Trp Asn Arg Gly Ile Ser	
130 135 140 145	
gct tgt gct gtt tgc gac gga gct gct ccg ata ttc cgt aac aaa cct	2037
Ala Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys Pro	
150 155 160	
ctt gcg gtg atc ggt gga ggc gat tca gca atg gaa gaa gca aac ttt	2085
Leu Ala Val Ile Gly Gly Gly Asp Ser Ala Met Glu Glu Ala Asn Phe	
165 170 175	
ctt aca aaa tat gga tct aaa gtg tat ata atc cat agg aga gat gct	2133
Leu Thr Lys Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp Ala	
180 185 190	
ttt aga gcg tct aag att atg cag cag cga gct ttg tct aat cct aag	2181
Phe Arg Ala Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro Lys	
195 200 205	
att gat gtg att tgg aac tcg tct gtt gtg gaa gct tat gga gat gga	2229
Ile Asp Val Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp Gly	
210 215 220 225	

gaa aga gat gtg ctt gga gga ttg aaa gtg aag aat gtg gtt acc gga 2277
 Glu Arg Asp Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr Gly
 230 235 240

gat gtt tct gat tta aaa gtt tct gga ttg ttc ttt gct att ggt cat 2325
 Asp Val Ser Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly His
 245 250 255

gag cca gct acc aag ttt ttg gat ggt ggt gtt gag tta gat tcg gat 2373
 Glu Pro Ala Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser Asp
 260 265 270

ggt tat gtt gtc acg aag cct ggt act aca cag act agc gtt ccc gga 2421
 Gly Tyr Val Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro Gly
 275 280 285

gtt ttc gct gcg ggt gat gtt cag gat aag aag tat agg caa gcc atc 2469
 Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala Ile
 290 295 300 305

act gct gca gga act ggg tgc atg gca gct ttg gat gca gag cat tac 2517
 Thr Ala Ala Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His Tyr
 310 315 320

tta caa gag att gga tct cag caa ggt aag agt gat tgaagcttaa 2563
 Leu Gln Glu Ile Gly Ser Gln Gln Gly Lys Ser Asp
 325 330

taagtatgaa ctaaaatgca tgtaggtgta agagctcatg gagagcatgg aatattgtat 2623

ccgaccatgt aacagtataa taactgagct ccactctact tcttctatga ataaacaaag 2683

gatgttatga tatattaaca ctctatctat gcaccttatt gttctatgat aaatttcctc 2743

ttattattat aaatcatctg aatcgtgacg gcttatggaa tgcttcaaata agtacaaaaa 2803

caaatgtgta ctataagact ttctaaacaa ttctaacttt agcattgtga acgagacata 2863

agtgттаага agacataaca attataatgg aagaagtttg tctccattta tatattatat 2923

attacccact tatgtattat attaggatgt taaggagaca taacaattat aaagagagaa 2983

gtttgtatcc atttatatat tatatactac ccatttatat attatactta tccacttatt 3043

taatgtcttt ataaggtttg atccatgata tttctaatat tttagttgat atgtatatga 3103

aagggtacta tttgaactct ctactctgt ataaaggttg gatcatcctt aaagtgggtc 3163

tatttaattt tattgcttct tacagataaa aaaaaaatta tgagttgggt tgataaaata 3223

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 gtttgctgca taatttatgc agtaaaacac tacacataac ctttttagca gtagagcaat 3643
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<210> 49

<211> 333

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Phaseolin
 promoter-thioredoxin reductase-phaseolin
 terminator

<400> 49

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Gly	Pro	Ala	Ala	His	Thr	Ala	Ala	Ile	Tyr	Ala	Ala	Arg	Ala	Glu	Leu	20	25	30	
Lys	Pro	Leu	Leu	Phe	Glu	Gly	Trp	Met	Ala	Asn	Asp	Ile	Ala	Pro	Gly	35	40	45	
Gly	Gln	Leu	Thr	Thr	Thr	Thr	Asp	Val	Glu	Asn	Phe	Pro	Gly	Phe	Pro	50	55	60	
Glu	Gly	Ile	Leu	Gly	Val	Glu	Leu	Thr	Asp	Lys	Phe	Arg	Lys	Gln	Ser	65	70	75	80
Glu	Arg	Phe	Gly	Thr	Thr	Ile	Phe	Thr	Glu	Thr	Val	Thr	Lys	Val	Asp	85	90	95	
Phe	Ser	Ser	Lys	Pro	Phe	Lys	Leu	Phe	Thr	Asp	Ser	Lys	Ala	Ile	Leu	100	105	110	
Ala	Asp	Ala	Val	Ile	Leu	Ala	Thr	Gly	Ala	Val	Ala	Lys	Arg	Leu	Ser	115	120	125	
Phe	Val	Gly	Ser	Gly	Glu	Gly	Ser	Gly	Gly	Phe	Trp	Asn	Arg	Gly	Ile	130	135	140	
Ser	Ala	Cys	Ala	Val	Cys	Asp	Gly	Ala	Ala	Pro	Ile	Phe	Arg	Asn	Lys	145	150	155	160
Pro	Leu	Ala	Val	Ile	Gly	Gly	Gly	Asp	Ser	Ala	Met	Glu	Glu	Ala	Asn	165	170	175	

Phe Leu Thr Lys Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp
 180 185 190
 Ala Phe Arg Ala Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro
 195 200 205
 Lys Ile Asp Val Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp
 210 215 220
 Gly Glu Arg Asp Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr
 225 230 235 240
 Gly Asp Val Ser Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly
 245 250 255
 His Glu Pro Ala Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser
 260 265 270
 Asp Gly Tyr Val Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro
 275 280 285
 Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala
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 Ile Thr Ala Ala Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His
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 Tyr Leu Gln Glu Ile Gly Ser Gln Gln Gly Lys Ser Asp
 325 330

<210> 50

<211> 4546

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Phaseolin
 promoter-oleosin thioredoxin reductase-phaseolin
 terminator

<220>

<221> CDS

<222> (1555) .. (1908)

<220>

<221> CDS

<222> (2149) .. (3312)

<400> 50

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 ttacttggtta ctttaatttc tcataatctt tggttgaaat tatcacgctt ccgcacacga 180
 tatccctaca aatttattat ttgttaaaca ttttcaaacc gcataaaatt ttatgaagtc 240


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ccgtctatct ttaatgtagt ctaacatttt catattgaaa tatataattt acttaatttt 300
agcgttggta gaaagcataa tgatttatto ttattcttct tcatataaat gttaaata 360
caatataaac aaattcttta ccttaagaag gatttcccat tttatatttt aaaaatatat 420
ttatcaaata tttttcaacc acgtaaactc cataataata agttgtttca aaagtaataa 480
aatttaactc cataattttt ttattcgact gatcttaaag caacacccag tgacacaact 540
agccattttt ttctttgaat aaaaaaatcc aattatcatt gtattttttt tatacaatga 600
aaatttcacc aaacaatcat ttgtggtatt tctgaagcaa gtcatgttat gcaaaattct 660
ataattccca ttgacacta cggaagtaac tgaagatctg cttttacatg cgagacacat 720
cttctaaagt aattttaata atagttacta tattcaagat ttcatatatc aaatactcaa 780
tattacttct aaaaaattaa ttagatataa ttaaaatatt acttttttaa ttttaagttt 840
aattgttgaa tttgtgacta ttgatttatt attctactat gtttaaattg ttttatagat 900
agtttaaagt aaatataagt aatgtagtag agtgtagag tgttacccta aaccataaac 960
tataagattt atggtggact aattttcata tatttcttat tgcttttacc ttttcttggg 1020
atgtaagtcc gtaactggaa ttactgtggg ttgccatggc actctgtggg cttttggttc 1080
atgcatggat gcttgcgcaa gaaaaagaca aagaacaaag aaaaaagaca aaacagagag 1140
acaaaacgca atcacacaac caactcaaat tagtcaactg ctgatcaaga tcgccgcgtc 1200
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actactctac tactataata cccaaccca actcatatc aatactactc tact atg 1557
                                     Met
                                     1

gcg gat aca gct aga gga acc cat cac gat atc atc ggc aga gac cag 1605
Ala Asp Thr Ala Arg Gly Thr His His Asp Ile Ile Gly Arg Asp Gln
                    5                      10                      15

tac ccg atg atg ggc cga gac cga gac cag tac cag atg tcc gga cga 1653
Tyr Pro Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met Ser Gly Arg
                20                      25                      30

gga tct gac tac tcc aag tct agg cag att gct aaa gct gca act gct 1701
Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr Ala
    35                      40                      45

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gtc aca gct ggt ggt tcc ctc ctt gtt ctc tcc agc ctt acc ctt gtt	1749
Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu Val	
50 55 60 65	
gga act gtc ata gct ttg act gtt gca aca cct ctg ctc gtt atc ttc	1797
Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile Phe	
70 75 80	
agc cca atc ctt gtc ccg gct ctc atc aca gtt gca ctc ctc atc acc	1845
Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile Thr	
85 90 95	
ggt ttt ctt tcc tct gga ggg ttt ggc att gcc gct ata acc gtt ttc	1893
Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val Phe	
100 105 110	
tct tgg att tac aag taagcacaca tttatcatct tacttcataa ttttgtgcaa	1948
Ser Trp Ile Tyr Lys	
115	
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cctagctagc ttgaatgtgt ctgtgtatat catctatata ggtaaaatgc ttggtatgat	2128
acctattgat tgtgaatagg tac gca acg gga gag cac cca cag gga tca gac	2181
Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp	
120 125	
aag ttg gac agt gca agg atg aag ttg gga agc aaa gct cag gat ctg	2229
Lys Leu Asp Ser Ala Arg Met Lys Leu Gly Ser Lys Ala Gln Asp Leu	
130 135 140 145	
aaa gac aga gct cag tac tac gga cag caa cat act ggt ggg gaa cat	2277
Lys Asp Arg Ala Gln Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His	
150 155 160	
gac cgt gac cgt act cgt ggt ggc cag cac act acc atg aat ggt ctc	2325
Asp Arg Asp Arg Thr Arg Gly Gly Gln His Thr Thr Met Asn Gly Leu	
165 170 175	
gaa act cac aac aca agg ctc tgt atc gta gga agt ggc cca gcg gca	2373
Glu Thr His Asn Thr Arg Leu Cys Ile Val Gly Ser Gly Pro Ala Ala	
180 185 190	
cac acg gcg gcg att tac gca gct agg gct gaa ctt aaa cct ctt ctc	2421
His Thr Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu Lys Pro Leu Leu	
195 200 205	
ttc gaa gga tgg atg gct aac gac atc gct ccc ggt ggt caa cta aca	2469
Phe Glu Gly Trp Met Ala Asn Asp Ile Ala Pro Gly Gly Gln Leu Thr	
210 215 220 225	
acc acc acc gac gtc gag aat ttc ccc gga ttt cca gaa ggt att ctc	2517
Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Pro Glu Gly Ile Leu	
230 235 240	

gga gta gag ctc act gac aaa ttc cgt aaa caa tcg gag cga ttc ggt	2565
Gly Val Glu Leu Thr Asp Lys Phe Arg Lys Gln Ser Glu Arg Phe Gly	
245 250 255	
act acg ata ttt aca gag acg gtg acg aaa gtc gat ttc tct tcg aaa	2613
Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp Phe Ser Ser Lys	
260 265 270	
ccg ttt aag cta ttc aca gat tca aaa gcc att ctc gct gac gct gtg	2661
Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu Ala Asp Ala Val	
275 280 285	
att ctc gct act gga gct gtg gct aag cgg ctt agc ttc gtt gga tct	2709
Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser Phe Val Gly Ser	
290 295 300 305	
ggt gaa ggt tct gga ggt ttc tgg aac cgt gga atc tcc gct tgt gct	2757
Gly Glu Gly Ser Gly Gly Phe Trp Asn Arg Gly Ile Ser Ala Cys Ala	
310 315 320	
gtt tgc gac gga gct gct ccg ata ttc cgt aac aaa cct ctt gcg gtg	2805
Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys Pro Leu Ala Val	
325 330 335	
atc ggt gga ggc gat tca gca atg gaa gaa gca aac ttt ctt aca aaa	2853
Ile Gly Gly Gly Asp Ser Ala Met Glu Glu Ala Asn Phe Leu Thr Lys	
340 345 350	
tat gga tct aaa gtg tat ata atc cat agg aga gat gct ttt aga gcg	2901
Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp Ala Phe Arg Ala	
355 360 365	
tct aag att atg cag cag cga gct ttg tct aat cct aag att gat gtg	2949
Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro Lys Ile Asp Val	
370 375 380 385	
att tgg aac tcg tct gtt gtg gaa gct tat gga gat gga gaa aga gat	2997
Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp Gly Glu Arg Asp	
390 395 400	
gtg ctt gga gga ttg aaa gtg aag aat gtg gtt acc gga gat gtt tct	3045
Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr Gly Asp Val Ser	
405 410 415	
gat tta aaa gtt tct gga ttg ttc ttt gct att ggt cat gag cca gct	3093
Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly His Glu Pro Ala	
420 425 430	
acc aag ttt ttg gat ggt ggt gtt gag tta gat tcg gat ggt tat gtt	3141
Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser Asp Gly Tyr Val	
435 440 445	
gtc acg aag cct ggt act aca cag act agc gtt ccc gga gtt ttc gct	3189
Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro Gly Val Phe Ala	
450 455 460 465	

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      470                      475                      480

gga act ggg tgc atg gca gct ttg gat gca gag cat tac tta caa gag 3285
Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His Tyr Leu Gln Glu
      485                      490                      495

att gga tct cag caa ggt aag agt gat tgaagcttaa taagtatgaa 3332
Ile Gly Ser Gln Gln Gly Lys Ser Asp
      500                      505

ctaaaatgca tgtaggtgta agagctcatg gagagcatgg aatattgtat ccgaccatgt 3392
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<210> 51
<211> 118

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<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Phaseolin
promoter-oleosin thioredoxin reductase-phaseolin
terminator

<400> 51

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Gln	Tyr	Pro	Met	Met	Gly	Arg	Asp	Arg	Asp	Gln	Tyr	Gln	Met	Ser	Gly
			20					25					30		
Arg	Gly	Ser	Asp	Tyr	Ser	Lys	Ser	Arg	Gln	Ile	Ala	Lys	Ala	Ala	Thr
		35					40					45			
Ala	Val	Thr	Ala	Gly	Gly	Ser	Leu	Leu	Val	Leu	Ser	Ser	Leu	Thr	Leu
	50					55					60				
Val	Gly	Thr	Val	Ile	Ala	Leu	Thr	Val	Ala	Thr	Pro	Leu	Leu	Val	Ile
65				70				75							80
Phe	Ser	Pro	Ile	Leu	Val	Pro	Ala	Leu	Ile	Thr	Val	Ala	Leu	Leu	Ile
			85					90						95	
Thr	Gly	Phe	Leu	Ser	Ser	Gly	Gly	Phe	Gly	Ile	Ala	Ala	Ile	Thr	Val
		100						105					110		
Phe	Ser	Trp	Ile	Tyr	Lys										
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<210> 52

<211> 388

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Phaseolin
promoter-oleosin thioredoxin reductase-phaseolin
terminator

<400> 52

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1				5					10					15	
Arg	Met	Lys	Leu	Gly	Ser	Lys	Ala	Gln	Asp	Leu	Lys	Asp	Arg	Ala	Gln
			20					25					30		
Tyr	Tyr	Gly	Gln	Gln	His	Thr	Gly	Gly	Glu	His	Asp	Arg	Asp	Arg	Thr
		35					40					45			
Arg	Gly	Gly	Gln	His	Thr	Thr	Met	Asn	Gly	Leu	Glu	Thr	His	Asn	Thr
	50					55					60				

Arg	Leu	Cys	Ile	Val	Gly	Ser	Gly	Pro	Ala	Ala	His	Thr	Ala	Ala	Ile	65	70	75	80
Tyr	Ala	Ala	Arg	Ala	Glu	Leu	Lys	Pro	Leu	Leu	Phe	Glu	Gly	Trp	Met	85	90	95	
Ala	Asn	Asp	Ile	Ala	Pro	Gly	Gly	Gln	Leu	Thr	Thr	Thr	Thr	Asp	Val	100	105	110	
Glu	Asn	Phe	Pro	Gly	Phe	Pro	Glu	Gly	Ile	Leu	Gly	Val	Glu	Leu	Thr	115	120	125	
Asp	Lys	Phe	Arg	Lys	Gln	Ser	Glu	Arg	Phe	Gly	Thr	Thr	Ile	Phe	Thr	130	135	140	
Glu	Thr	Val	Thr	Lys	Val	Asp	Phe	Ser	Ser	Lys	Pro	Phe	Lys	Leu	Phe	145	150	155	160
Thr	Asp	Ser	Lys	Ala	Ile	Leu	Ala	Asp	Ala	Val	Ile	Leu	Ala	Thr	Gly	165	170	175	
Ala	Val	Ala	Lys	Arg	Leu	Ser	Phe	Val	Gly	Ser	Gly	Glu	Gly	Ser	Gly	180	185	190	
Gly	Phe	Trp	Asn	Arg	Gly	Ile	Ser	Ala	Cys	Ala	Val	Cys	Asp	Gly	Ala	195	200	205	
Ala	Pro	Ile	Phe	Arg	Asn	Lys	Pro	Leu	Ala	Val	Ile	Gly	Gly	Gly	Asp	210	215	220	
Ser	Ala	Met	Glu	Glu	Ala	Asn	Phe	Leu	Thr	Lys	Tyr	Gly	Ser	Lys	Val	225	230	235	240
Tyr	Ile	Ile	His	Arg	Arg	Asp	Ala	Phe	Arg	Ala	Ser	Lys	Ile	Met	Gln	245	250	255	
Gln	Arg	Ala	Leu	Ser	Asn	Pro	Lys	Ile	Asp	Val	Ile	Trp	Asn	Ser	Ser	260	265	270	
Val	Val	Glu	Ala	Tyr	Gly	Asp	Gly	Glu	Arg	Asp	Val	Leu	Gly	Gly	Leu	275	280	285	
Lys	Val	Lys	Asn	Val	Val	Thr	Gly	Asp	Val	Ser	Asp	Leu	Lys	Val	Ser	290	295	300	
Gly	Leu	Phe	Phe	Ala	Ile	Gly	His	Glu	Pro	Ala	Thr	Lys	Phe	Leu	Asp	305	310	315	320
Gly	Gly	Val	Glu	Leu	Asp	Ser	Asp	Gly	Tyr	Val	Val	Thr	Lys	Pro	Gly	325	330	335	
Thr	Thr	Gln	Thr	Ser	Val	Pro	Gly	Val	Phe	Ala	Ala	Gly	Asp	Val	Gln	340	345	350	
Asp	Lys	Lys	Tyr	Arg	Gln	Ala	Ile	Thr	Ala	Ala	Gly	Thr	Gly	Cys	Met	355	360	365	

Ala Ala Leu Asp Ala Glu His Tyr Leu Gln Glu Ile Gly Ser Gln Gln
 370 375 380

Gly Lys Ser Asp
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<210> 53
 <211> 4545
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Phaseolin
 promoter-thioredoxin reductase oleosin-phaseolin
 terminator

<220>
 <221> CDS
 <222> (1555)..(2907)

<220>
 <221> CDS
 <222> (3148)..(3312)

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 tatccctaca aatttattat ttgttaaaca ttttcaaacc gcataaaatt ttatgaagtc 240
 ccgtctatct ttaatgtagt ctaacatttt catattgaaa tatataattt acttaatttt 300
 agcgttggtta gaaagcataa tgatttattc ttattcttct tcatataaat gtttaatatata 360
 caatataaac aaattcttta ccttaagaag gatttcccat tttatatttt aaaaatatat 420
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 aatttaactc cataattttt ttattcgact gatcttaaag caacaccag tgacacaact 540
 agccattttt ttctttgaat aaaaaaatcc aattatcatt gtattttttt tatacaatga 600
 aaatttcacc aaacaatcat ttgtggtatt tctgaagcaa gtcattgtat gcaaaattct 660
 ataattccca ttgacacta cggaagtaac tgaagatctg cttttacatg cgagacacat 720
 cttctaaagt aattttaata atagttacta tattcaagat ttcatatata aaataactcaa 780
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 agtttaaagt aaatataagt aatgtagtag agtgtagtag tgttacccta aaccataaac 960

tataagattt atggtggact aattttcata tattttcttat tgcttttacc ttttcttggt	1020
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acaaaacgca atcacacaac caactcaaat tagtcactgg ctgatcaaga tcgccgcgtc	1200
catgtatgtc taaatgccat gcaaagcaac acgtgcttaa catgcacttt aaatgggtca	1260
cccatctcaa cccacacaca aacacattgc ctttttcttc atcatcacca caaccacctg	1320
tatatattca ttctcttccg ccacctcaat ttcttcactt caacacacgt caacctgcat	1380
atgcgtgtca tcccatgccc aaatctccat gcatgttcca accaccttct ctcttatata	1440
atacctataa atacctctaa tatcactcac ttctttcatc atccatccat ccagagtact	1500
actactctac tactataata ccccaaccca actcatattc aatactactc tact atg	1557
	Met
	1
aat ggt ctc gaa act cac aac aca agg ctc tgt atc gta gga agt ggc	1605
Asn Gly Leu Glu Thr His Asn Thr Arg Leu Cys Ile Val Gly Ser Gly	
5 10 15	
cca gcg gca cac acg gcg gcg att tac gca gct agg gct gaa ctt aaa	1653
Pro Ala Ala His Thr Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu Lys	
20 25 30	
cct ctt ctc ttc gaa gga tgg atg gct aac gac atc gct ccc ggt ggt	1701
Pro Leu Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala Pro Gly Gly	
35 40 45	
caa cta aca acc acc acc gac gtc gag aat ttc ccc gga ttt cca gaa	1749
Gln Leu Thr Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Pro Glu	
50 55 60 65	
ggg att ctc gga gta gag ctc act gac aaa ttc cgt aaa caa tcg gag	1797
Gly Ile Leu Gly Val Glu Leu Thr Asp Lys Phe Arg Lys Gln Ser Glu	
70 75 80	
cga ttc ggt act acg ata ttt aca gag acg gtg acg aaa gtc gat ttc	1845
Arg Phe Gly Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp Phe	
85 90 95	
tct tcg aaa ccg ttt aag cta ttc aca gat tca aaa gcc att ctc gct	1893
Ser Ser Lys Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu Ala	
100 105 110	
gac gct gtg att ctc gct act gga gct gtg gct aag cgg ctt agc ttc	1941
Asp Ala Val Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser Phe	
115 120 125	
gtt gga tct ggt gaa ggt tct gga ggt ttc tgg aac cgt gga atc tcc	1989
Val Gly Ser Gly Glu Gly Ser Gly Gly Phe Trp Asn Arg Gly Ile Ser	
130 135 140 145	

gct tgt gct gtt tgc gac gga gct gct ccg ata ttc cgt aac aaa cct	2037
Ala Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys Pro	
150 155 160	
ctt gcg gtg atc ggt gga ggc gat tca gca atg gaa gaa gca aac ttt	2085
Leu Ala Val Ile Gly Gly Gly Asp Ser Ala Met Glu Glu Ala Asn Phe	
165 170 175	
ctt aca aaa tat gga tct aaa gtg tat ata atc cat agg aga gat gct	2133
Leu Thr Lys Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp Ala	
180 185 190	
ttt aga gcg tct aag att atg cag cag cga gct ttg tct aat cct aag	2181
Phe Arg Ala Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro Lys	
195 200 205	
att gat gtg att tgg aac tcg tct gtt gtg gaa gct tat gga gat gga	2229
Ile Asp Val Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp Gly	
210 215 220 225	
gaa aga gat gtg ctt gga gga ttg aaa gtg aag aat gtg gtt acc gga	2277
Glu Arg Asp Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr Gly	
230 235 240	
gat gtt tct gat tta aaa gtt tct gga ttg ttc ttt gct att ggt cat	2325
Asp Val Ser Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly His	
245 250 255	
gag cca gct acc aag ttt ttg gat ggt ggt gtt gag tta gat tcg gat	2373
Glu Pro Ala Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser Asp	
260 265 270	
ggt tat gtt gtc acg aag cct ggt act aca cag act agc gtt ccc gga	2421
Gly Tyr Val Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro Gly	
275 280 285	
gtt ttc gct gcg ggt gat gtt cag gat aag aag tat agg caa gcc atc	2469
Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala Ile	
290 295 300 305	
act gct gca gga act ggg tgc atg gca gct ttg gat gca gag cat tac	2517
Thr Ala Ala Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His Tyr	
310 315 320	
tta caa gag att gga tct cag caa ggt aag agt gat atg gcg gat aca	2565
Leu Gln Glu Ile Gly Ser Gln Gln Gly Lys Ser Asp Met Ala Asp Thr	
325 330 335	
gct aga gga acc cat cac gat atc atc ggc aga gac cag tac ccg atg	2613
Ala Arg Gly Thr His His Asp Ile Ile Gly Arg Asp Gln Tyr Pro Met	
340 345 350	
atg ggc cga gac cga gac cag tac cag atg tcc gga cga gga tct gac	2661
Met Gly Arg Asp Arg Asp Gln Tyr Gln Met Ser Gly Arg Gly Ser Asp	
355 360 365	

tac tcc aag tct agg cag att gct aaa gct gca act gct gtc aca gct 2709
 Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr Ala Val Thr Ala
 370 375 380 385

ggt ggt tcc ctc ctt gtt ctc tcc agc ctt acc ctt gtt gga act gtc 2757
 Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu Val Gly Thr Val
 390 395 400

ata gct ttg act gtt gca aca cct ctg ctc gtt atc ttc agc cca atc 2805
 Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile Phe Ser Pro Ile
 405 410 415

ctt gtc ccg gct ctc atc aca gtt gca ctc ctc atc acc ggt ttt ctt 2853
 Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile Thr Gly Phe Leu
 420 425 430

tcc tct gga ggg ttt ggc att gcc gct ata acc gtt ttc tct tgg att 2901
 Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val Phe Ser Trp Ile
 435 440 445

tac aag taagcacaca tttatcatct tacttcataa ttttgtgcaa tatgtgcatg 2957
 Tyr Lys
 450

catgtgttga gccagtagct ttggatcaat ttttttggtc gaataacaaa tgtaacaata 3017

agaaattgca aattctaggg aacatttggg taactaaata cgaaatttga cctagctagc 3077

ttgaatgtgt ctgtgtatat catctatata ggtaaaatgc ttggtatgat acctattgat 3137

tgtgaatagg tac gca acg gga gag cac cca cag gga tca gac aag ttg 3186
 Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp Lys Leu
 455 460

gac agt gca agg atg aag ttg gga agc aaa gct cag gat ctg aaa gac 3234
 Asp Ser Ala Arg Met Lys Leu Gly Ser Lys Ala Gln Asp Leu Lys Asp
 465 470 475 480

aga gct cag tac tac gga cag caa cat act ggt ggg gaa cat gac cgt 3282
 Arg Ala Gln Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp Arg
 485 490 495

gac cgt act cgt ggt ggc cag cac act act taagcttaat aagtatgaac 3332
 Asp Arg Thr Arg Gly Gly Gln His Thr Thr
 500 505

taaaatgcat gtaggtgtaa gagctcatgg agagcatgga atattgtatc cgaccatgta 3392

acagtataat aactgagctc catctcactt cttctatgaa taaacaaagg atgttatgat 3452

atattaacac tctatctatg caccttattg ttctatgata aatttcctct tattattata 3512

aatcatctga atcgtgacgg cttatggaat gcttcaaata gtacaaaaac aaatgtgtac 3572

tataagactt tctaaacaat tctaacttta gcattgtgaa cgagacataa gtgttaagaa 3632

gacataacaa ttataatgga agaagtttgt ctccatttat atattatata ttaccactt 3692

atgtattata ttaggatgtt aaggagacat aacaattata aagagagaag tttgtatcca 3752
 tttatatatt atatactacc catttatata ttatacttat ccacttattt aatgtcttta 3812
 taaggtttga tccatgatat ttctaattt ttagttgata tgtatatgaa agggactat 3872
 ttgaactctc ttactctgta taaagggttg atcatcctta aagtgggtct atttaatttt 3932
 attgcttctt acagataaaa aaaaaattat gagttgggtt gataaaatat tgaaggattt 3992
 aaaataataa taaataataa ataacatata atatatgtat ataaatttat tataatataa 4052
 catttatcta taaaaaagta aatattgtca taaatctata caatcggtta gccttgctgg 4112
 acgactctca attattttaa cgagagtaaa catatttgac tttttgggta ttttaacaaat 4172
 tattatttaa cactatatga aatTTTTTTTT ttttatcggc aaggaaataa aattaaatta 4232
 ggagggacaa tgggtgtgtcc caatccttat acaaccaact tccacaggaa ggtcaggtcg 4292
 gggacaacaa aaaaacaggc aagggaatt ttttaatttg ggttgtcttg tttgctgcat 4352
 aatttatgca gtaaaacact acacataacc ctttttagcag tagagcaatg gttgaccgtg 4412
 tgcttagctt cttttatttt atttttttat cagcaaagaa taaataaaat aaaatgagac 4472
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<210> 54

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Phaseolin
 promoter-thioredoxin reductase oleosin-phaseolin
 terminator

<400> 54

Met	Asn	Gly	Leu	Glu	Thr	His	Asn	Thr	Arg	Leu	Cys	Ile	Val	Gly	Ser
1				5					10					15	
Gly	Pro	Ala	Ala	His	Thr	Ala	Ala	Ile	Tyr	Ala	Ala	Arg	Ala	Glu	Leu
			20					25					30		
Lys	Pro	Leu	Leu	Phe	Glu	Gly	Trp	Met	Ala	Asn	Asp	Ile	Ala	Pro	Gly
		35					40					45			
Gly	Gln	Leu	Thr	Thr	Thr	Thr	Asp	Val	Glu	Asn	Phe	Pro	Gly	Phe	Pro
	50					55					60				
Glu	Gly	Ile	Leu	Gly	Val	Glu	Leu	Thr	Asp	Lys	Phe	Arg	Lys	Gln	Ser
65					70					75					80

Glu	Arg	Phe	Gly	Thr	Thr	Ile	Phe	Thr	Glu	Thr	Val	Thr	Lys	Val	Asp	85	90	95
Phe	Ser	Ser	Lys	Pro	Phe	Lys	Leu	Phe	Thr	Asp	Ser	Lys	Ala	Ile	Leu	100	105	110
Ala	Asp	Ala	Val	Ile	Leu	Ala	Thr	Gly	Ala	Val	Ala	Lys	Arg	Leu	Ser	115	120	125
Phe	Val	Gly	Ser	Gly	Glu	Gly	Ser	Gly	Gly	Phe	Trp	Asn	Arg	Gly	Ile	130	135	140
Ser	Ala	Cys	Ala	Val	Cys	Asp	Gly	Ala	Ala	Pro	Ile	Phe	Arg	Asn	Lys	145	150	155
Pro	Leu	Ala	Val	Ile	Gly	Gly	Gly	Asp	Ser	Ala	Met	Glu	Glu	Ala	Asn	165	170	175
Phe	Leu	Thr	Lys	Tyr	Gly	Ser	Lys	Val	Tyr	Ile	Ile	His	Arg	Arg	Asp	180	185	190
Ala	Phe	Arg	Ala	Ser	Lys	Ile	Met	Gln	Gln	Arg	Ala	Leu	Ser	Asn	Pro	195	200	205
Lys	Ile	Asp	Val	Ile	Trp	Asn	Ser	Ser	Val	Val	Glu	Ala	Tyr	Gly	Asp	210	215	220
Gly	Glu	Arg	Asp	Val	Leu	Gly	Gly	Leu	Lys	Val	Lys	Asn	Val	Val	Thr	225	230	235
Gly	Asp	Val	Ser	Asp	Leu	Lys	Val	Ser	Gly	Leu	Phe	Phe	Ala	Ile	Gly	245	250	255
His	Glu	Pro	Ala	Thr	Lys	Phe	Leu	Asp	Gly	Gly	Val	Glu	Leu	Asp	Ser	260	265	270
Asp	Gly	Tyr	Val	Val	Thr	Lys	Pro	Gly	Thr	Thr	Gln	Thr	Ser	Val	Pro	275	280	285
Gly	Val	Phe	Ala	Ala	Gly	Asp	Val	Gln	Asp	Lys	Lys	Tyr	Arg	Gln	Ala	290	295	300
Ile	Thr	Ala	Ala	Gly	Thr	Gly	Cys	Met	Ala	Ala	Leu	Asp	Ala	Glu	His	305	310	315
Tyr	Leu	Gln	Glu	Ile	Gly	Ser	Gln	Gln	Gly	Lys	Ser	Asp	Met	Ala	Asp	325	330	335
Thr	Ala	Arg	Gly	Thr	His	His	Asp	Ile	Ile	Gly	Arg	Asp	Gln	Tyr	Pro	340	345	350
Met	Met	Gly	Arg	Asp	Arg	Asp	Gln	Tyr	Gln	Met	Ser	Gly	Arg	Gly	Ser	355	360	365
Asp	Tyr	Ser	Lys	Ser	Arg	Gln	Ile	Ala	Lys	Ala	Ala	Thr	Ala	Val	Thr	370	375	380

Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu Val Gly Thr
 385 390 395 400

Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile Phe Ser Pro
 405 410 415

Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile Thr Gly Phe
 420 425 430

Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val Phe Ser Trp
 435 440 445

Ile Tyr Lys
 450

<210> 55

<211> 55

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Phaseolin
 promoter-thioredoxin reductase oleosin-phaseolin
 terminator

<400> 55

Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp Lys Leu Asp Ser Ala
 1 5 10 15

Arg Met Lys Leu Gly Ser Lys Ala Gln Asp Leu Lys Asp Arg Ala Gln
 20 25 30

Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp Arg Asp Arg Thr
 35 40 45

Arg Gly Gly Gln His Thr Thr
 50 55